

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/628,693

DATE: 08/28/2001
TIME: 08:20:34

Input Set : A:\34950193.app
Output Set: N:\CRF3\08282001\I628693.raw

3 <110> APPLICANT: Haroche, Julien
4 Allignet, Jeanine
5 El Solh, Nevine
7 <120> TITLE OF INVENTION: DETECTION OF A GENE, vatD, ENCODING AN ACETYLTRANSFERASE
8 INACTIVATING STREPTOGRAMIN
10 <130> FILE REFERENCE: 03495.0193
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/628,693
C--> 13 <141> CURRENT FILING DATE: 2000-07-28
15 <160> NUMBER OF SEQ ID NOS: 22
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 213
21 <212> TYPE: PRT
22 <213> ORGANISM: Enterococcus faecium
24 <400> SEQUENCE: 1
25 Met Thr Ile Pro Asp Ala Asn Ala Ile Tyr His Asn Ser Ala Ile Lys
26 1 5 10 15
28 Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile
29 20 25 30
31 Gly Asp Tyr Thr Tyr Tyr Asp Asp Pro Val Asn Pro Thr Asp Phe Glu
32 35 40 45
34 Lys His Val Thr His His Tyr Glu Phe Leu Gly Asp Lys Leu Ile Ile
35 50 55 60
37 Gly Lys Phe Cys Ser Leu Ala Ser Gly Ile Glu Phe Ile Met Asn Gly
38 65 70 75 80
40 Ala Asn His Val Met Lys Gly Ile Ser Thr Tyr Pro Phe Asn Ile Leu
41 85 90 95
43 Gly Gly Asp Trp Gln Gln Tyr Thr Pro Glu Leu Thr Asp Leu Pro Leu
44 100 105 110
46 Lys Gly Asp Thr Val Val Gly Asn Asp Val Trp Phe Gly Gln Asn Val
47 115 120 125
49 Thr Val Leu Pro Gly Val Lys Ile Gly Asp Gly Ala Ile Ile Gly Ala
50 130 135 140
52 Asn Ser Val Val Thr Lys Asp Val Ala Pro Tyr Thr Ile Val Gly Gly
53 145 150 155 160
55 Asn Pro Ile Gln Leu Ile Gly Pro Arg Phe Glu Pro Glu Val Ile Gln
56 165 170 175
58 Ala Leu Glu Asn Leu Ala Trp Trp Asn Lys Asp Ile Glu Trp Ile Thr
59 180 185 190
61 Ala Asn Val Pro Lys Leu Met Gln Thr Thr Pro Thr Leu Glu Leu Ile
62 195 200 205
64 Asn Ser Leu Met Glu
65 210
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 642
70 <212> TYPE: DNA
71 <213> ORGANISM: Enterococcus faecium

ENTERED

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73 <400> SEQUENCE: 2
74 atgactatac ctgacgaaaa tgcaatctat cataaactcag ccatcaaaga ggttgtcttt 60
75 atcaagaacg tgatcaaaaag tcccaatatt gaaattgggg actacaccta ttatgatgac 120
76 ccagtaaattc ccaccgatil iygyaaacac gttaccatc actatgaatt tctagggcgc 180
77 aaattaatca tcggtaaatt ttgttctctc gccagtgcca ttgaatttat catgaacgg 240
78 gccaaccacg taatgaaagg tatttcgact tatccattt atatattagg tggcgattgg 300
79 caacaataca ctcctgaact gactgatttgc ccgttggaaag gtgatactgt agtcgaaat 360
80 gacgtgttgt ttgggcaaaa tggaccgtc ctaccaggcg taaaatagg tgacgtgccc 420
81 attatcgag caaatgtgt tgtaacaaaa gacgtcgctc catatacaat tgcgtggc 480
82 aatccaaattc aactcatcg accaagattt gaaaccggaaat ttattcaaggc attagaaaat 540
83 ctggcatggt ggaataaaga tattgaatgg ataactgcta atgttcctaa actaatgcaa 600
84 aacaacacccca cacttgaatt gataaacagt ttaatggaaa aa 642
87 <210> SEQ ID NO: 3
88 <211> LENGTH: 25
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
95 <400> SEQUENCE: 3 25
96 caatatttggg attcgggact acacc
99 <210> SEQ ID NO: 4
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
107 <400> SEQUENCE: 4 22
108 ctgtttatga attcaagtgt gg
111 <210> SEQ ID NO: 5
112 <211> LENGTH: 7
113 <212> TYPE: PRT
114 <213> ORGANISM: Enterococcus faecium
116 <400> SEQUENCE: 5
117 Ile Met Asn Gly Ala Asn His
118 1 5
121 <210> SEQ ID NO: 6
122 <211> LENGTH: 18
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
129 <220> FEATURE:
130 <223> OTHER INFORMATION: "n" bases may be a, t, c or g
132 <400> SEQUENCE: 6 18
133 atthatgaayg cnaaycay
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 5
138 <212> TYPE: PRT
139 <213> ORGANISM: Enterococcus faecium

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141 <400> SEQUENCE: 7
142 Gly Asn Asp Val Trp
143 1 5
146 <210> SEQ ID NO: 8
147 <211> LENGTH: 15
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
154 <220> FEATURE:
155 <223> OTHER INFORMATION: "n" bases may be a, t, c or g
157 <400> SEQUENCE: 8
WQ4> 158 ccanacrtcr ttncc 15
161 <210> SEQ ID NO: 9
162 <211> LENGTH: 8
163 <212> TYPE: PRT
164 <213> ORGANISM: Enterococcus faecium
166 <400> SEQUENCE: 9
167 Ala Asn Ala Ile Tyr His Asn Ser
168 1 5
171 <210> SEQ ID NO: 10
172 <211> LENGTH: 24
173 <212> TYPE: DNA
174 <213> ORGANISM: Enterococcus faecium
176 <400> SEQUENCE: 10 24
177 gcaaatgcaa tctatcataa ctca
180 <210> SEQ ID NO: 11
181 <211> LENGTH: 9
182 <212> TYPE: PRT
183 <213> ORGANISM: Enterococcus faecium
185 <400> SEQUENCE: 11
186 Met Gln Thr Thr Pro Thr Leu Glu Leu
187 1 5
190 <210> SEQ ID NO: 12
191 <211> LENGTH: 27
192 <212> TYPE: DNA
193 <213> ORGANISM: Enterococcus faecium
195 <400> SEQUENCE: 12
196 atgcaaacaa caccacact tgaattg 27
199 <210> SEQ ID NO: 13
200 <211> LENGTH: 23
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
207 <400> SEQUENCE: 13
208 tagaaagaat tcagtgattg tgg 23
211 <210> SEQ ID NO: 14
212 <211> LENGTH: 26

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213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
219 <400> SEQUENCE: 14
220 ggattcacta aatagtaaag gccgtg 26
223 <210> SEQ ID NO: 15
224 <211> LENGTH: 840
225 <212> TYPE: DNA
226 <213> ORGANISM: Enterococcus faecium
228 <400> SEQUENCE: 15
229 aaatttaggc gcacaaaaaag aaagagtgtg acaaaaacatg gttatgctac atgtttaagg 60
230 taaaaatagt tatgtcacaa ctacttattt ttttacccaa tcttctagac tataattaaa 120
231 attaaataac tcaattcggg ggtactaacc tgactatacc tgacgcaa at gcaatctatc 180
232 ataactcagc catcaaagag gttgacttta tcaagaacgt gatcaaaatg cccaatattg 240
233 aaattggggg ctacacccat tatgtatgacc cagtaaatcc caccgattt gagaaacacg 300
234 ttacccatca ctatgaattt cttaggcgaca aattaatcat cggtaaat tt tgttctctcg 360
235 ccagtggcat tgaatttatac atgaacgggtg ccaaccacgt aatgaaaggt atttcgactt 420
236 atccatttaa tatatttaggt ggcgattggc aacaatacac tcctgaactg actgatttgc 480
237 cgttgaagg tgatactgta gtcggaaatg acgtgtggtt tggcaaaat gtgaccgtcc 540
238 taccaggcggtt aaaaataggt gacgggtgcca ttatcgagc aaatagtgtt gtaacaaaag 600
239 acgtcgctcc atatacaatt gtcgggtggca atccaattca actcatcgga ccaagattt 660
240 aaccggaaagt tattcaagca tttagaaaatc tggcatgggtt gaaataagat attgaatgga 720
241 taactgctaa ttttctaaa ctaatgc aacacccac acttgaattt gataaacagtt 780
242 taatggaaaa ataaaaacaa aaaagccgtg caagcaatcc aaaaatgatt gtttacacgg 840
245 <210> SEQ ID NO: 16
246 <211> LENGTH: 44
247 <212> TYPE: DNA
248 <213> ORGANISM: Enterococcus faecium
250 <400> SEQUENCE: 16
251 tgcacaaact acttattttt ttacccaaatc ttcttagacta taat 44
254 <210> SEQ ID NO: 17
255 <211> LENGTH: 1080
256 <212> TYPE: DNA
257 <213> ORGANISM: Enterococcus faecium
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (271)..(912)
263 <400> SEQUENCE: 17
264 ccctttaaag agggcttttataattaaatc acaaatcaact tatcacaat cacaagtgtat 60
266 ttgtgattgt tgatgataaa ataagaataa gaagaaatag aaagaagtgtt gtgattgtgg 120
268 gaaatttagg cgacaaaaaa gaaagagtgtt gacaaaacat gttatgctt catgtttaag 180
270 gtaaaaaatag ttatgtcaca actacttatt ttttacccaa atcttctaga ctataattaa 240
272 aattaaataaa ctcaattcgg aggtactaacc atg act ata cct gac gca aat gca 294
273 Met Thr Ile Pro Asp Ala Asn Ala
274 1 5
276 atc tat cat aac tca gcc atc aaa gag gtt gtc ttt atc aag aac gtg 342
277 Ile Tyr His Asn Ser Ala Ile Lys Glu Val Val Phe Ile Lys Asn Val
278 10 15 20

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280 atc aaa agt ccc aat att gaa att ggg gac tac acc tat tat gat gac	390
281 Ile Lys Ser Pro Asn Ile Glu Ile Gly Asp Tyr Thr Tyr Tyr Asp Asp	
282 25 30 35 40	
284 cca gta aat ccc acc gat ttt gag aaa cac gtt acc cat cac tat gaa	438
285 Pro Val Asn Pro Thr Asp Phe Glu Lys His Val Thr His His Tyr Glu	
286 45 50 55	
288 ttt cta ggc gac aaa tta atc atc ggt aaa ttt tgt tct ctc gcc agt	486
289 Phe Leu Gly Asp Lys Leu Ile Ile Gly Lys Phe Cys Ser Leu Ala Ser	
290 60 65 70	
292 ggc att gaa ttt atc atg aac ggt gcc aac cac gta atg aaa ggt att	534
293 Gly Ile Glu Phe Ile Met Asn Gly Ala Asn His Val Met Lys Gly Ile	
294 75 80 85	
296 tcg act tat cca ttt aat ata tta ggt ggc gat tgg caa caa tac act	582
297 Ser Thr Tyr Pro Phe Asn Ile Leu Gly Gly Asp Trp Gln Gln Tyr Thr	
298 90 95 100	
300 cct gaa ctg act gat ttg ccg ttg aaa ggt gat act gta gtc gga aat	630
301 Pro Glu Leu Thr Asp Leu Pro Leu Lys Gly Asp Thr Val Val Gly Asn	
302 105 110 115 120	
304 gac gtg tgg ttt ggg caa aat gtg acc gtc cta cca ggc gta aaa ata	678
305 Asp Val Trp Phe Gly Gln Asn Val Thr Val Leu Pro Gly Val Lys Ile	
306 125 130 135	
308 ggt gac ggt gcc att atc gga gca aat agt gtt gta aca aaa gac gtc	726
309 Gly Asp Gly Ala Ile Ile Gly Ala Asn Ser Val Val Thr Lys Asp Val	
310 140 145 150	
312 gct cca tat aca att gtc ggt ggc aat cca att caa ctc atc gga cca	774
313 Ala Pro Tyr Thr Ile Val Gly Gly Asn Pro Ile Gln Leu Ile Gly Pro	
314 155 160 165	
316 aga ttt gaa ccg gaa gtt att caa gca tta gaa aat ctg gca tgg tgg	822
317 Arg Phe Glu Pro Glu Val Ile Gln Ala Leu Glu Asn Leu Ala Trp Trp	
318 170 175 180	
320 aat aaa gat att gaa tgg ata act gct aat gtt cct aaa cta atg caa	870
321 Asn Lys Asp Ile Glu Trp Ile Thr Ala Asn Val Pro Lys Leu Met Gln	
322 185 190 195 200	
324 aca aca ccc aca ctt gaa ttg ata aac agt tta atg gaa aaa	912
325 Thr Thr Pro Thr Leu Glu Leu Ile Asn Ser Leu Met Glu Lys	
326 205 210	
328 taaaaacaaa aaagccgtgc aagcaatcca aaaatgattt tttacacggc ctttactatt	972
330 tagtgaatcc aatttattaa taatagatat gatataccag taaaaaatac actagccacc	1032
332 tctggcggta ctctactcgt atatttatt tacgaccttc tgatgata	1080
335 <210> SEQ ID NO: 18	
336 <211> LENGTH: 214	
337 <212> TYPE: PRT	
338 <213> ORGANISM: Enterococcus faecium	
340 <400> SEQUENCE: 18	
341 Met Thr Ile Pro Asp Ala Asn Ala Ile Tyr His Asn Ser Ala Ile Lys	
342 1 5 10 15	
344 Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile	
345 20 25 30	
347 Gly Asp Tyr Thr Tyr Asp Asp Pro Val Asn Pro Thr Asp Phe Glu	

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:133 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:133 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:158 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:158 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8